

Sequence Listing

<100> Kurume University

<120> Gene mina53 involved in cancer, Protein Mina53 and
Monoclonal Antibody Thereof

<130> JFH15228-PCT

<160> 3

<210> 1

<211> 464

<212> DNA

<213> Homo sapiens

<400>1

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Met Pro Lys Lys Ala Lys Pro Thr Gly Ser Gly Lys Glu Glu Gly Pro Ala Pro
      5              10              15

tgt aag cag atg aag tta gaa gca gct ggg ggg cct tca gct tta aac ttt gac
Cys Lys Gln Met Lys leu Glu Ala Ala Gly Gly Pro Ser Ala Leu Asn Phe Asp
    20              25              30              35

agt ccc agt agt ctc ttt gaa agt tta atc tcg ccc atc aag aca gag act ttt
Ser Pro Ser Ser Leu Phe Glu Ser Leu Ile Ser Pro Ile Lys Thr Glu Thr Phe
      40              45              50

ttc aag gaa ttc tgg gag cag aag ccc ctt ctc att cag aga gat gac cct gca
Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu Leu Ile Gln Arg Asp Asp Pro Ala
    55              60              65              70

ctg gcc aca tac tat ggg tcc ctg ttc aag cta aca gat ctg aag agt ctg tgc
Leu Ala Thr Tyr Tyr Gly Ser Leu Phe Lys Leu Thr Asp Leu Lys Ser Leu Cys
      75              80              85              90

agc cgg ggg atg tac tat gga aga gat gtg aat gtc tgc cgg tgt gtc aat ggg
Ser Arg Gly Met Tyr Tyr Gly Arg Asp Val Asn Val Cys Arg Cys Val Asn Gly
      95              100             105

aag aag aag gtt tta aat aaa gat ggc aaa gca cac ttt ctt cag ctg aga aaa
Lys Lys Lys Val Leu Asn Lys Asp Gly Lys Ala His Phe Leu Gln Leu Arg Lys
    110              115              120              125

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gat ttt gat cag aaa agg gca acg att cag ttt cac caa cct cag aga ttt aag
 Asp Phe Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Phe Lys
 130 135 140

gat gag ctt tgg agg atc cag gag aag ctg gaa tgt tac ttt ggc tcc ttg gtt
 Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser Leu Val
 145 150 155 160

ggc tcg aat gtg tac ata act ccc gca gga tct cag ggc ctg ccg ccc cat tat
 Gly Ser Asn Val Tyr Ile Thr Pro Ala Gly Ser Gln Gly Leu Pro Pro His Tyr
 165 170 175 180

gat gat gtc gag gtt ttc atc ctg cag ctg gag gga gag aaa cac tgg cgc ctc
 Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly Glu Lys His Trp Arg Leu
 185 190 195

tac cac ccc act gtg ccc ctg gca cga gag tac agc gtg gag gcc gag gaa agg
 Tyr His Pro Thr Val Pro Leu Ala Arg Glu Tyr Ser Val Glu Ala Glu Glu Arg
 200 205 210 215

atc ggc agg ccg gtg cat gag ttt atg ctg aag ccg ggt gat ttg ttg tac ttt
 Ile Gly Arg Pro Val His Glu Phe Met Leu Lys Pro Gly Asp Leu Leu Tyr Phe
 220 225 230

ccc aga gga acc att cat caa gcg gac act cct gcg ggg ctg gcc cac tcg act
 Pro Arg Gly Thr Ile His Gln Ala Asp Thr Pro Ala Gly Leu Ala His Ser Thr
 235 240 245 250

cac gtg acc atc agc acc tac cag aac aat tca tgg gga gat ttc ctt ttg gat
 His Val Thr Ile Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Phe Leu Leu Asp
 255 260 265 270

acc atc tcg ggg ctt gta ttt gat act gca aag gaa gac gtg gag tta cgg acc
 Thr Ile Ser Gly Leu Val Phe Asp Thr Ala Lys Glu Asp Val Glu Leu Arg Thr
 275 280 285

ggc ata ccc cgg cag ctg ctc ctg gtg gaa tcc aca act gtt gct aca aga cga
 Gly Ile Pro Arg Gln Leu Leu Leu Val Glu Ser Thr Thr Val Ala Thr Arg Arg
 290 295 300 305

tta agt ggc ttc ctg agg aca ctt gca gac cgg ctg gag ggc acc aaa gaa ctg
 Leu Ser Gly Phe Leu Arg Thr Leu Ala Asp Arg Leu Glu Gly Thr Lys Glu Leu
 310 315 320

ctt tcc tca gac atg aag aag gat ttt att atg cac aga ctc ccc cct tac tct
 Leu Ser Ser Asp Met Lys Lys Asp Phe Ile Met His Arg Leu Pro Pro Tyr Ser
 325 330 335 340

gcg gga gat ggg gca gag ctg tca aca cca ggt gga aag tta ccg agg ctg gac
 Ala Gly Asp Gly Ala Glu Leu Ser Thr Pro Gly Gly Lys Leu Pro Arg Leu Asp
 345 350 355 360

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agt gta gtg aga ctg cag ttt aaa gac cac att gtc ctc aca gta ctg ccg gat
Ser Val Val Arg Leu Gln Phe Lys Asp His Ile Val Leu Thr Val Leu Pro Asp
365 370 375

caa gat caa tct gat gaa gct caa gaa aag atg gtg tac atc tat cat tcc tta
Gln Asp Gln Ser Asp Glu Ala Gln Glu Lys Met Val Tyr Ile Tyr His Ser Leu
380 385 390 395

aag aat agt aga gag aca cac atg atg gga aat gag gag gaa aca gag ttt cat
Lys Asn Ser Arg Glu Thr His Met Met Gly Asn Glu Glu Glu Thr Glu Phe His
400 405 410

gga ctt cgc ttc cct ttg tca cat ttg gat gca ctg aag caa att tgg aat agt
Gly Leu Arg Phe Pro Leu Ser His Leu Asp Ala Leu Lys Gln Ile Trp Asn Ser
415 420 425 430

cca gct att tct gtc aag gac ctg aaa ctt act aca gat gag gaa aag gaa agc
Pro Ala Ile Ser Val Lys Asp Leu Lys Leu Thr Thr Asp Glu Glu Lys Glu Ser
435 440 445 450

ctg gta tta tcc ctc tgg aca gaa tgt tta att caa gta gtc tag
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455 460 464

<210> 2

<211> 465

<212> DNA

<213> Mus musculus

<400> 2

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5 10 15

tgc aag cgg gtg aag gag gag ctg cct gaa acg ctt tct gta tta aac ttt gac
Cys Lys Arg Val Lys Glu Glu Leu Pro Glu Thr Leu Ser Val Leu Asn Phe Asp
20 25 30 35

agc ccc agt agt ttc ttc gaa agt tta atc tca ccc atc aaa gta gag act ttt
Ser Pro Ser Ser Phe Phe Glu Ser Leu Ile Ser Pro Ile Lys Val Glu Thr Phe
40 45 50

ttc aag gaa ttc tgg gaa caa aag ccc ctt ctc att cag agg gat gac cct gta
Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu Leu Ile Gln Arg Asp Asp Pro Val
55 60 65 70

ctg gcc aaa tat tac cag tct ctg ttc agc ctc tca gat ctg aag aga ctc tgc
Leu Ala Lys Tyr Tyr Gln Ser Leu Phe Ser Leu Ser Asp Leu Lys Arg Leu Cys

75	80	85	90
aag aaa gga gtg tac tat gga aga gac gtg aat gtc tgc cgg agc atc agt ggg			
Lys Lys Gly Val Tyr Tyr Gly Arg Asp Val Asn Val Cys Arg Ser Ile Ser Gly			
95	100	105	
aag aag aag gtt tta aat aag gat ggc aga gca cat ttt ctt cag ctg aga aaa			
Lys Lys Lys Val Leu Asn Lys Asp Gly Arg Ala His Phe Leu Gln Leu Arg Lys			
110	115	120	125
gat ttt gat cag aag agg gca aca att cag ttt cac caa cct cag aga tat aag			
Asp Phe Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Tyr Lys			
130	135	140	
gat gag ctg tgg cgg atc cag gaa aag ctg gaa tgt tac ttt ggg tcc tta gta			
Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser Leu Val			
145	150	155	160
ggc tcg aat gtg tac atg act cct gca gga tct cag ggc ctc cct cca cat tat			
Gly Ser Asn Val Tyr Met Thr Pro Ala Gly Ser Gln Gly Leu Pro Pro His Tyr			
165	170	175	180
gat gat gtt gag gtt ttt atc ctg cag ctg gag gga acg aaa cac tgg cgc ctg			
Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly Thr Lys His Trp Arg Leu			
185	190	195	
tac tcc cca act gtg ccc ctg gca cac gag tac agt gtg gaa tct gag gac cgg			
Tyr Ser Pro Thr Val Pro Leu Ala His Glu Tyr Ser Val Glu Ser Glu Asp Arg			
200	205	210	215
atc ggc aca ccg aca cac gac ttc ctg ctg aag cct gga gat ttg ttg tac ttt			
Ile Gly Thr Pro Thr His Asp Phe Leu Leu Lys Pro Gly Asp Leu Leu Tyr Phe			
220	225	230	
ccc aga ggg acc att cat cag gca gaa act cct tca ggc ctg gcc tac tct att			
Pro Arg Gly Thr Ile His Gln Ala Glu Thr Pro Ser Gly Leu Ala Tyr Ser Ile			
235	240	245	250
cac ctg act att agc acc tac cag aac aat tca tgg gga gac tgc ctt ttg gat			
His Leu Thr Ile Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Cys Leu Leu Asp			
255	260	265	270
tcc att tcg ggg ttc gta ttt gac att gca aag gaa gat gtg gca tta agg agt			
Ser Ile Ser Gly Phe Val Phe Asp Ile Ala Lys Glu Asp Val Ala Leu Arg Ser			
275	280	285	
gga atg ccc cgg cgg atg ctc ctg aat gtg gaa acc cca gct gat gta aca agg			
Gly Met Pro Arg Arg Met Leu Leu Asn Val Glu Thr Pro Ala Asp Val Thr Arg			
290	295	300	305
aag ttg agt ggc ttt ctg agg act ctt gca gac cag ctc gag ggc aga gaa gag			
Lys Leu Ser Gly Phe Leu Arg Thr Leu Ala Asp Gln Leu Glu Gly Arg Glu Glu			

310

315

320

ctg ctg tca tca gat atg aag aag gac ttc gtc aag cac aga ctc cct cct ttc
 Leu Leu Ser Ser Asp Met Lys Lys Asp Phe Val Lys His Arg Leu Pro Pro Phe
 325 330 335 340

ttc gag gga aat gga acg gag acg atg gac cca ggt aaa cag ttg cca agg ttg
 Phe Glu Gly Asn Gly Thr Glu Thr Met Asp Pro Gly Lys Gln Leu Pro Arg Leu
 345 350 355 360

gac aac ata ata aga ctg cag ttc aaa gat cac att gtc ctc aca gta ggg cca
 Asp Asn Ile Ile Arg Leu Gln Phe Lys Asp His Ile Val Leu Thr Val Gly Pro
 365 370 375

gat aag aat cca ttt gat gaa gct caa caa aag gtg gtt tac atc tat cat tct
 Asp Lys Asn Pro Phe Asp Glu Ala Gln Gln Lys Val Val Tyr Ile Tyr His Ser
 380 385 390 395

ctg aag aat gtg agg cag atg cac atg ata gga gaa gag gag gaa tcc gag att
 Leu Lys Asn Val Arg Gln Met His Met Ile Gly Glu Glu Glu Glu Ser Glu Ile
 400 405 410

ttc ggt ctt cgc ttt cct tta tca cat gtg gat gct ctg aag caa atc tgg tgc
 Phe Gly Leu Arg Phe Pro Leu Ser His Val Asp Ala Leu Lys Gln Ile Trp Cys
 415 420 425 430

ggg tca cca att cgt gtt aag gaa ctg aaa ctt gac aca gat gaa gaa aag gag
 Gly Ser Pro Ile Arg Val Lys Glu Leu Lys Leu Asp Thr Asp Glu Glu Lys Glu
 435 440 445 450

aac ctg gca ctg tct ctc tgg tcg gag tct tta atc caa gta ctc tag
 Asn Leu Ala Leu Ser Leu Trp Ser Glu Ser Leu Ile Gln Val Leu ***
 455 460 465

<210> 3

<211> 475

<212> DNA

<213> Rattus norvegicus

<400> 3

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tgc aag cag gtg aaa gag gag cta cct aat acg ctt tct gta tta aac ttt gac
 Cys Lys Gln Val Lys Glu Glu Leu Pro Asn Thr Leu Ser Val Leu Asn Phe Asp
 20 25 30 35

agc ccc agt agt ttc ttt gaa agt tta ata tca ccc atc aaa gta gag aca ttt

Ser	Pro	Ser	Ser	Phe	Phe	Glu	Ser	Leu	Ile	Ser	Pro	Ile	Lys	Val	Glu	Thr	Phe
			40					45					50				
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Phe	Lys	Glu	Phe	Trp	Glu	Gln	Lys	Pro	Leu	Leu	Ile	Gln	Arg	Asp	Asp	Pro	Ser
55					60				65						70		
ctg	gcc	gca	tat	tac	cag	tct	ctg	ttc	agc	ctc	tca	gat	ctg	agg	agt	ctc	tgc
Leu	Ala	Ala	Tyr	Tyr	Gln	Ser	Leu	Phe	Ser	Leu	Ser	Asp	Leu	Arg	Ser	Leu	Cys
		75					80				85						90
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Ser	Gln	Gly	Leu	Tyr	Tyr	Gly	Arg	Asp	Val	Asn	Val	Cys	Arg	Cys	Ile	Gly	Gly
				95					100					105			
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Lys	Lys	Lys	Val	Leu	Asn	Lys	Asp	Gly	Lys	Ala	Gln	Phe	Leu	Gln	Leu	Arg	Lys
	110					115				120						125	
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Asp	Phe	Asp	Gln	Lys	Arg	Ala	Thr	Ile	Gln	Phe	His	Gln	Pro	Gln	Arg	Phe	Lys
			130					135				140					
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Asp	Glu	Leu	Trp	Arg	Ile	Gln	Glu	Lys	Leu	Glu	Cys	Tyr	Phe	Gly	Ser	Leu	Val
145				150					155					160			
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Gly	Ser	Asn	Val	Tyr	Met	Thr	Pro	Ala	Gly	Ser	Gln	Gly	Leu	Pro	Pro	His	Tyr
		165					170				175						180
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Asp	Asp	Val	Glu	Val	Phe	Ile	Leu	Gln	Leu	Glu	Gly	Arg	Lys	Arg	Trp	Arg	Leu
			185					190					195				
tac	tcc	cca	act	gtg	ccc	ctg	gcg	cgt	gag	tac	agt	gtg	gag	cct	gag	gac	cgg
Tyr	Ser	Pro	Thr	Val	Pro	Leu	Ala	Arg	Glu	Tyr	Ser	Val	Glu	Pro	Glu	Asp	Arg
	200					205				210						215	
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			220					225					230				
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235					240					245				250			
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His	Leu	Thr	Ile	Ser	Thr	Tyr	Gln	Asn	Asn	Ser	Trp	Gly	Asp	Tyr	Leu	Leu	Asp
		255					260					265					270
tcc	att	tcg	ggg	ctt	gta	ttt	gac	att	gca	aag	gaa	gat	gtg	gca	tta	agg	act

Ser	Ile	Ser	Gly	Leu	Val	Phe	Asp	Ile	Ala	Lys	Glu	Asp	Val	Ala	Leu	Arg	Thr
				275					280					285			
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290				295				300				305					
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Lys	Leu	Ser	Gly	Phe	Leu	Arg	Thr	Leu	Ala	Asp	Gln	Leu	Glu	Gly	Arg	Lys	Glu
310				315				320									
ctg	ctc	tca	tca	gat	atg	aag	aag	gac	ttc	gtc	atg	cac	aga	ctt	ccc	cct	ttc
Leu	Leu	Ser	Ser	Asp	Met	Lys	Lys	Asp	Phe	Val	Met	His	Arg	Leu	Pro	Pro	Phe
325				330				335				340					
tgt	gtg	gga	aat	gga	aca	gag	tca	atg	aac	cca	ggg	gga	aag	ttg	cca	agg	ttg
Cys	Val	Gly	Asn	Gly	Thr	Glu	Ser	Met	Asn	Pro	Gly	Gly	Lys	Leu	Pro	Arg	Leu
345				350				355				360					
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Asn	Ser	Ile	Val	Arg	Leu	Gln	Phe	Lys	Asp	His	Ile	Val	Leu	Thr	Val	Gly	Pro
365				370				375									
gat	cag	aat	caa	tct	gat	gaa	gct	caa	caa	aag	gtg	gtt	tac	atc	tac	cat	tct
Asp	Gln	Asn	Gln	Ser	Asp	Glu	Ala	Gln	Gln	Lys	Val	Val	Tyr	Ile	Tyr	His	Ser
380				385				390				395					
cta	aag	aat	gag	aga	cag	acg	cac	atg	atg	ggg	aaa	gag	gtg	gaa	aca	gag	att
Leu	Lys	Asn	Glu	Arg	Gln	Thr	His	Met	Met	Gly	Lys	Glu	Val	Glu	Thr	Glu	Ile
400				405				410									
tat	gga	ctt	cgc	ttt	cct	tta	tcc	tat	gtg	gac	gct	ctg	aag	caa	atc	tgg	tgc
Tyr	Gly	Leu	Arg	Phe	Pro	Leu	Ser	Tyr	Val	Asp	Ala	Leu	Lys	Gln	Ile	Trp	Cys
415				420				425				430					
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435				440				445				450					
aac	ctg	gca	gtg	tct	ctc	tgg	aca	gag	tgt	cta	gtc	cac	gtg	ctc	tag		
Asn	Leu	Ala	Val	Ser	Leu	Trp	Thr	Glu	Cys	Leu	Val	His	Val	Leu	***		
455				460				465									